

1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60  
1 M S S R I A R A L A L V V T L L H L T R 20

61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120  
21 L A L S T C P A A C H C P L E A P K C A 40

121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180  
41 P G V G L V R D G C G C C K V C A K Q L 60

181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240  
61 N E D C S K T Q P C D H T K G L E C N F 80

241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300  
81 G A S S T A L K G I C R A Q S E G R P C 100

301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360  
101 E Y N S R I Y Q N G E S F Q P N C K H Q 120

361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCAAGAACTATCTCTC 420  
121 C T C I D G A V G C I P L C P Q E L S L 140

421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480  
141 P N L G C P N P R L V K V T G Q C C E E 160

**FIG. 1A**

481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540  
161 W V C D E D S I K D P M E D Q D G L L G 180

541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600  
181 K E L G F D A S E V E L T R N N E L I A 200

601 GTTGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGAATGGAGCCTCGCATCCTA 660  
201 V G K G S S L K R L P V F G M E P R I L 220

661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACCTTCATGGTCCCAGTGCTCA 720  
221 Y N P L Q G Q K C I V Q T T S W S Q C S 240

721 AAGACCTGTGGAACCTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780  
241 K T C G T G I S T R V T N D N P E C R L 260

781 GTGAAAGAAACCCGATTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840  
261 V K E T R I C E V R P C G Q P V Y S S L 280

841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTACTTAC 900  
281 K K G K K C S K T K K S P E P V R F T Y 300

901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTGCGTGGACGGC 960  
301 A G C L S V K K Y R P K Y C G S C V D G 320

FIG. 1B

961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020  
321 R C C T P Q L T R T V K M R F R C E D G 340

1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAAC TGCCCG 1080  
341 E T F S K N V M M I Q S C K C N Y N C P 360

1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140  
361 H A N E A A F P F Y R L F N D I H K F R 380

1141 GACTAA 1146  
381 D \* 382

**FIG. 1C**